STIC Database Tracking Number 151799

TO: Nita M Minnifield Location: Rem-3C01&3C18 Art Unit: 1645 Wednesday, April 27, 2005 **Case Serial Number: 09/508967**	**From:** Toby Port **Location:** Biotech-Chem Library REM1-A59 **Phone:** 272-2523 toby.port@uspto.gov

Search Notes

Dear Examiner Minnifield,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

Reviewed
5/5/05
MM

sira
Search and Information
Resources Administration

151739

CRFC

From:	Chan, Christina
Sent:	Tuesday, April 26, 2005 2:09 PM
To:	Minnifield, Nita; STIC-Biotech/ChemLib
Subject:	RE: rush sequence search

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----
From:	Minnifield, Nita
Sent:	Tuesday, April 26, 2005 7:10 AM
To:	Chan, Christina
Subject:	rush sequence search

Christina, please approve, 2 month amdt.

STIC

09/508967

Please do a commercial and interference sequence search on SEQ ID NO: 1 of the above application.

Please search aa 1-415 of SEQ ID NO: 1 and aa 79-415 of SEQ ID NO: 1.

Please provide a paper copy of the results.

Thanks,
Minnifield
71976

OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: April 26, 2005, 18:03:03 / Search time 31.4383 Seconds
                                              (without alignments)
                                              3567.329 Million cell updates/sec

Title: US-09-508-967-1_COPY_79_415
Perfect score: 1884
Sequence: 1 PCKKDGKGNDVDRFSVKEQA.........GSYENWIDNQRKQFDKQKKY 337

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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    14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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    17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
    18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
    19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
    20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	885	47.0	2710	13	US-10-153-273-12	Sequence 12, Appl
2	845	44.9	700	13	US-10-153-273-10	Sequence 10, Appl
3	653	34.7	3542	15	US-10-087-013-2	Sequence 2, Appl
4	379.5	20.1	362	13	US-10-087-013-18	Sequence 18, Appl
5	360.5	19.1	411	13	US-10-153-273-19	Sequence 19, Appl
6	308.5	16.4	1143	9	US-09-924-154-14	Sequence 14, Appl
7	281	14.9	1435	13	US-10-153-273-4	Sequence 4, Appl
8	280.5	14.9	749	13	US-10-153-273-6	Sequence 6, Appl
9	280.5	14.9	1086	9	US-09-924-154-15	Sequence 15, Appl
10	270	14.3	616	15	US-10-293-913A-4	Sequence 4, Appl
11	269	14.3	616	15	US-10-293-913A-2	Sequence 2, Appl
12	269	14.3	1421	9	US-09-924-154-13	Sequence 13, Appl
13	241	12.8	921	13	US-09-153-273-8	Sequence 8, Appl
14	235	12.5	972	9	US-09-924-154-16	Sequence 16, Appl
15	229.5	12.2	311	15	US-10-087-013-10	Sequence 10, Appl
16	220	12.2	407	15	US-10-087-013-8	Sequence 8, Appl
17	218	11.7	308	15	US-10-087-013-11	Sequence 11, Appl
18	216.5	11.6	1501	9	US-09-924-154-17	Sequence 17, Appl
19	216.5	11.5	1568	17	US-10-712-533A-12	Sequence 12, Appl
20	213.5	11.3	351	15	US-10-087-013-9	Sequence 9, Appli
21	207	11.0	1115	13	US-10-153-273-2	Sequence 2, Appli
22	205	10.9	294	15	US-10-087-013-7	Sequence 7, Appli
23	197.5	10.5	411	13	US-10-153-273-20	Sequence 20, Appli
24	159.5	8.5	282	13	US-10-153-273-16	Sequence 16, Appli
25	158.5	8.4	277	13	US-10-153-273-15	Sequence 15, Appli
26	128.5	6.8	448	14	US-10-153-668-370	Sequence 370, Appl
27	126	6.7	291	13	US-10-153-273-13	Sequence 13, Appli
28	121	6.4	311	13	US-10-153-273-21	Sequence 21, Appli
29	117.5	6.2	754	14	US-10-153-668-254	Sequence 254, Appl
30	115.5	6.1	281	13	US-10-153-273-1	Sequence 1, Appli
31	115	6.1	324	13	US-10-153-273-17	Sequence 17, Appli
32	111	5.9	1257	16	US-10-408-765A-1486	Sequence 1486, Ap
33	108	5.7	665	10	US-09-820-843A-107	Sequence 107, App
34	107.5	5.7	1064	14	US-10-424-599-145507	Sequence 145507,
35	107	5.7	284	15	US-10-424-599-144189	Sequence 144189,
36	106.5	5.7	1002	15	US-10-654-616-4	Sequence 4, Appli
37	105	5.6	1154	10	US-09-963-137-203	Sequence 203, App
38	105	5.6	1154	10	US-09-962-854A-4	Sequence 4, Appli
39	105	5.6	1154	10	US-09-963-131-203	Sequence 203, App
40	104.5	5.5	294	15	US-10-424-599-237559	Sequence 237559,
41	104.5	5.5	1429	10	US-09-953-407-1	Sequence 1, Appli
42	102.5	5.4	905	16	US-10-437-963-152106	Sequence 152106,
43	102	5.4	905	16	US-09-925-300-1496	Sequence 1496, Ap
44	102	5.4	578	9	US-10-104-047-3843	Sequence 3843, Ap
45	102	5.4	1179	9	US-09-821-883-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-10-153-273-12
Sequence 12, Application US/10153273
Publication No. US20020169305A1
GENERAL INFORMATION:

APPLICANT: Sim, Kim L.
           Chitnis, Chetan
           Miller, Louis H.
           Peterson, David S.
           Su, Xin-zhuan
           Wellems, Thomas E.

TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
           AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:
    ADDRESSEE: Knobbe Martens Olson & Bear
    STREET: 620 Newport Center Drive 16th Floor
    CITY: Newport Beach
    STATE: California
    COUNTRY: US
    ZIP: 92660

COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/10/153,273
    FILING DATE: 21-May-2002
    CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/09/210,288
    FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
    NAME: Fuller, Michael
    REGISTRATION NUMBER: 36,516

OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: April 26, 2005, 17:50:53 ; Search time 9.16007 Seconds
(without alignments)
2746.348 Million cell updates/sec

Title: 1884
Perfect score: 1884
Sequence: 1 PCKKDGKGNDVDRFSVKEQA..........GSYENWIDNQRKQFDKQKKY 337

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
Listing first 45 summaries

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Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	885	47.0	3060	2	US-08-568-459A-16	Sequence 16, Appl
6	845	44.9	700	2	US-08-487-826B-14	Sequence 14, Appl
7	845	44.9	700	2	US-08-568-459A-10	Sequence 10, Appl
8	845	44.9	700	3	US-08-487-826B-10	Sequence 10, Appl
9	845	44.9	700	3	US-09-210-288-10	Sequence 10, Appl
10	379.5	20.1	362	2	US-08-568-459A-18	Sequence 18, Appl
11	379.5	20.1	362	2	US-08-487-826B-30	Sequence 30, Appl
12	360.5	19.1	362	3	US-09-210-288-18	Sequence 18, Appl
13	360.5	19.1	411	2	US-08-568-459A-19	Sequence 19, Appl
14	360.5	19.1	411	2	US-08-487-826B-31	Sequence 31, Appl
15	281	14.9	1435	2	US-08-568-459A-4	Sequence 4, Appl
16	281	14.9	1435	2	US-08-487-826B-4	Sequence 4, Appl
17	281	14.9	1435	3	US-09-210-288-4	Sequence 4, Appl
18	280.5	14.9	749	2	US-08-568-459A-6	Sequence 6, Appl
19	280.5	14.9	749	2	US-08-487-826B-6	Sequence 6, Appl
20	280.5	14.9	749	3	US-09-210-288-6	Sequence 6, Appl
21	241	12.8	921	2	US-08-568-459A-8	Sequence 8, Appl
22	241	12.8	921	2	US-08-487-826B-8	Sequence 8, Appl
23	241	12.8	921	3	US-09-210-288-8	Sequence 8, Appl
24	207	11.0	1115	2	US-08-568-459A-2	Sequence 2, Appl
25	207	11.0	1115	2	US-08-487-826B-2	Sequence 2, Appl
26	207	11.0	1115	3	US-09-210-288-2	Sequence 2, Appl
27	207	11.0	1115	6	5198347-6	Patent No. 5198347
28	207	11.0	1115	6	5198347-6	Patent No. 5198347
29	197.5	10.5	411	2	US-08-568-459A-20	Sequence 20, Appl
30	197.5	10.5	411	2	US-08-487-826B-32	Sequence 32, Appl
31	197.5	10.5	411	3	US-09-210-288-20	Sequence 20, Appl
32	159.5	8.5	282	2	US-08-568-459A-16	Sequence 16, Appl
33	159.5	8.5	282	2	US-08-487-826B-28	Sequence 28, Appl
34	159.5	8.5	282	3	US-09-210-288-16	Sequence 16, Appl
35	158.5	8.4	277	2	US-08-568-459A-15	Sequence 15, Appl
36	158.5	8.4	277	2	US-08-487-826B-27	Sequence 27, Appl
37	158.5	8.4	277	3	US-09-210-288-15	Sequence 15, Appl
38	150	8.0	197	6	5198347-4	Patent No. 5198347
39	150	8.0	197	6	5198347-2	Patent No. 5198347
40	150	8.0	778	6	5198347-4	Patent No. 5198347
41	150	8.0	778	6	5198347-2	Patent No. 5198347
42	126	6.7	291	2	US-08-568-459A-25	Sequence 25, Appl
43	126	6.7	291	2	US-08-487-826B-25	Sequence 25, Appl
44	126	6.7	291	3	US-09-210-288-13	Sequence 13, Appl
45	121	6.4	311	2	US-08-568-459A-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-487-826B-16
Sequence 16, Application US/08487826B
Patent No. 5993827

GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhuan
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2182 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-487-826B-16

Query Match 47.4%; Score 892.5; DB 2; Length 2182;

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                          GenCore version 5.1.6
                     Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:          April 26, 2005, 17:50:52 ; Search time 40.9376 Seconds
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Title:           US-09-508-967-1_COPY_79_415
Perfect score:   1884
Sequence:        1 PCKKDGKGNDVDRFSVKEQA...........GSYENWIDNQRKQFDKQKKY 337

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:    1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
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Database :       UniProt_03:*
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                 2:  uniprot_trembl:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES

Result            %      Query
No.    Score   Match  Length  DB  ID         Description
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Result No.	Score	% Match	Query Length	DB	ID	Description
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3	1123.5	59.6	2215	2	Q8IK37	Q8IK37 plasmodium
4	1085.5	57.6	2215	2	Q8IBX3	Q8IBX3 plasmodium
5	1039.5	55.2	2215	2	Q8IBW9	Q8IBW9 plasmodium
6	1020.5	54.2	2264	2	Q9U0G6	Q9U0G6 plasmodium
7	1003.5	53.3	2152	2	Q8I2E3	Q8I2E3 plasmodium
8	1003.5	53.3	2201	2	Q8IFQ6	Q8IFQ6 plasmodium
9	994	52.8	2267	2	Q8IFQ5	Q8IFQ5 plasmodium
10	992.5	52.7	2326	2	Q8IBX1	Q8IBX1 plasmodium
11	991.5	52.6	2149	2	Q8IV6	Q8IV6 plasmodium
12	988	52.4	2192	2	Q8IFK7	Q8IFK7 plasmodium
13	945.5	50.2	2192	2	Q8IBW7	Q8IBW7 plasmodium
14	935.5	49.7	2312	2	Q9U0G5	Q9U0G5 plasmodium
15	926	49.2	2231	2	Q8IV7	Q8IV7 plasmodium
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18	903.5	48.0	2265	2	Q8IS19	Q8IS19 plasmodium
19	903.5	48.0	2710	2	Q8IAS3	Q8IAS3 plasmodium
20	894	47.5	2710	2	Q9XZB8	Q9XZB8 plasmodium
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27	879	46.7	3954	2	Q26031	Q26031 plasmodium
28	872	46.3	2287	2	Q6LEV2	Q6LEV2 plasmodium
29	868.5	46.1	1711	2	Q8I520	Q8I520 plasmodium
30	868	46.1	1729	2	Q96108	Q96108 plasmodium
31	868	46.1	2924	2	Q25733	Q25733 plasmodium
32	863	45.8	2135	2	O61077	O61077 plasmodium
33	858.5	45.6	2223	2	Q8IDI2	Q8IDI2 plasmodium
34	854.5	45.4	2241	2	Q8IK37	Q8IK37 plasmodium
35	846.5	44.9	3026	2	Q26030	Q26030 plasmodium
36	840.5	44.6	896	2	Q86MR4	Q86MR4 plasmodium
37	834.5	44.3	2169	2	Q97312	Q97312 plasmodium
38	833.5	44.2	2256	2	Q8IS15	Q8IS15 plasmodium
39	824.5	43.8	2270	2	Q8IBW8	Q8IBW8 plasmodium
40	823.5	43.7	2239	2	Q8IAK1	Q8IAK1 plasmodium
41	818	43.4	2268	2	Q8I4N5	Q8I4N5 plasmodium
42	806.5	42.8	2120	2	Q8I4N5	Q8I4N5 plasmodium
43	806	42.8	2595	2	Q8IBD8	Q8IBD8 plasmodium
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45	794.5	42.2	2209	2	O97324	O97324 plasmodium

ALIGNMENTS

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AC   O60991;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Erythrocyte membrane protein 1.
GN   Name=PCR3S1.2-var1;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Chen Q.J., Wahlgren M.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99080592; PubMed=9419207;
RA   Chen Q., Barragan A., Fernandez V., Sundstrom A., Schlichtherle M.,
RA   Sahlen A., Carlson J., Datta S., Wahlgren M.;
RT   "Identification of Plasmodium falciparum erythrocyte membrane protein
RT   1 (PfEMP1) as the rosetting ligand of the malaria parasite P.
RT   falciparum.";
RL   J. Exp. Med. 187:15-23(1998).
SQ   SEQUENCE   2228 AA;   5D8C89BFA22DC8B CRC64;

Query Match      99.6%;    Score 1876;   DB 2;   Length 2228;
Best Local Similarity    99.7%;   Pred. No. 3.8e-126;
Matches   336;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db   199 KKKKQNGKETERECLEQKLKEIFKKIHDNLKDKEAQKRYNGDEDPNFYKLREDWWTANRE 258

Qy   181 TVWGAMTCSKELDNSSYFRATCNDTGQGPSQTHNKCRCDKDKGANAGKPKAGDGDVTIVP 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   259 TVWGAMTCSKELDNSSYFRATCNDTGQGPSQTHNKCRCDKDKGANAGKPKAGDGDVTIVP 318

Qy   241 TYFDVPQYLRWFEEWAEDFCRKKKKKKLENLEKQCRGDKDKSDEYRYCSRNGYDCEQTISR 300
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OM protein - protein search, using sw model

Run on: April 26, 2005, 17:50:53 ; Search time 6.55906 Seconds
                                                 (without alignments)
                                                 4943.551 Million cell updates/sec

Title: US-09-508-967-1_COPY_79_415
Perfect score: 1884
Sequence: 1 PCKKDGKGNDVDRFSVKEQA.........GSYENWIDNQRKQFDKQKKY 337
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_79:*
              1: pir1:*
              2: pir2:*
              3: pir3:*
              4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1876	99.6	2228	2	T14029	variant-specific s
2	894	47.5	2197	2	B71600	variant-specific s
3	892.5	47.4	2182	2	T28634	variant-specific s
4	885	47.0	3078	2	T28432	variant-specific s
5	868.5	46.1	1711	2	C71625	variant-specific s
6	868	46.1	1729	2	T18396	erythrocyte membra
7	868	46.1	2924	2	T18378	variant-specific s
8	863	45.8	2135	2	T14602	variant-specific s
9	846.5	44.9	3026	2	T28431	variant-specific s
10	789	41.9	2647	2	T28161	variant surface pr
11	775	41.1	2212	2	T28157	hypothetical prote
12	759	40.3	2664	2	T28626	erythrocyte membra
13	707.5	37.6	3006	2	T28625	variant-specific s
14	680	36.1	2042	2	T18399	variant-specific s
15	633.5	33.6	2706	2	T28155	variant-specific s
16	281	14.9	1435	2	A37793	erythrocyte-bindin
17	207.5	11.0	1045	2	T18373	erythrocyte bindin
18	207	11.0	1070	2	T30848	Duffy receptor - P
19	186.5	9.9	1153	2	T28652	erythrocyte bindin
20	150	8.0	778	2	A35970	erythrocyte-bindin
21	117.5	6.2	754	1	JC5514	CDC28/cdc2-like ki
22	114	6.1	1282	2	JE0120	glycoprotein A - m
23	111	5.9	1257	1	I58383	retinoblastoma bin
24	111	5.9	1608	2	T13216	minor capsid prote
25	110.5	5.9	807	2	T18454	hypothetical prote
26	108	5.7	665	2	B71609	hypothetical prote
27	108	5.7	4981	2	T18489	hypothetical prote
28	107	5.7	1199	2	JC4816	major surface glyc
29	106.5	5.7	590	2	A25680	nuclear histone-bi
30	106.5	5.7	710	1	I51283	hepatocyte growth
31	106.5	5.7	1002	2	T30546	major surface glyc
32	106.5	5.7	2441	2	D71623	erythrocyte membra
33	106	5.6	508	2	B71620	hypothetical prote
34	104.5	5.5	2116	2	A26655	hypothetical prote
35	104	5.5	710	2	T12487	zinc finger protei
36	102.5	5.4	829	2	I46668	myosin heavy chain
37	101.5	5.4	2010	2	B71616	hypothetical prote
38	101	5.4	520	2	A39577	DNA topoisomerase
39	101.5	5.4	1390	2	S51364	protein-tyrosine k
40	101	5.4	1154	2	A31491	sperm tail-specifi
41	100	5.3	783	2	T18477	sex-determining re
42	100	5.3	2523	2	A45509	hypothetical prote
43	99.5	5.3	359	2	A47437	B cell differentia
44	99.5	5.2	4753	1	A47437	LDL-receptor-relat
45	98.5	5.2	649	2	T37740	coiled-coil protei

ALIGNMENTS

RESULT 1
T14029
variant-specific surface protein 1 - malaria parasite (Plasmodium falciparum)
N;Alternate names: erythrocyte membrane binding protein 1 (EMP1)
N;Species: Plasmodium falciparum
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14029
R;Chen, Q.; Barragan, A.; Fernandez, V.; Sundstrom, A.; Schlichtherle, M.; Sahlen, A.;
J. Exp. Med. 187, 15-23, 1998
A;Title: Identification of Plasmodium falciparum erythrocyte membrane protein 1 (PfEMP1)
A;Reference number: Z17860; MUID:98080592; PMID:9419207
A;Accession: T14029
A;Molecule type: mRNA
A;Residues: 1-2228 <CHE>
A;Cross-references: UNIPROT:O60991; EMBL:AF003473; NID:g2961467; PID:g2961468; PIDN:AAC
A;Genetic:
A;Note: FCR3S1.2-var1
A;Status: preliminary; translated from GB/EMBL/DDBJ

Query Match   99.6%;   Score 1876; DB 2;   Length 2228;
Best Local Similarity   99.7%;   Pred. No. 4.2e-124;
Matches 336;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy   1 PCKKDGKGNDVDRFSVKEQAGYDNRKCMKCGSNGMTCAPFRRIHLCNKNFPNMNSNDSSKAK 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   79 PCKKDGKGNDVDRFSVKEQAGYDNRKCMKCGSNGMTCAPFRRIHLCNKNFPNMNSNDSSKAK 138

Qy   61 HDLLAEVCMAAKYEGBSIKTHYPKYDSKYPGSDFPMCTMLARSFADIGDIIRGRDLYLGN 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   139 HDLLAEVCMAAKYEGBSIKTHYPKYDSKYPGSDFPMCTMLARSFADIGDIIRGRDLYLGN 198

Qy   121 KKKKKONGKETEREKLEQKLKEIFKKIIHDNLKDKEAQKRYNGDEDPNFYKLREDWTANRE 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   199 KKKKKONGKETEREKLEQKLKEIFKKIIHDNLKDKEAQKRYNGDEDPNFYKLREDWTANRE 258

Qy   181 TVWGAMTCSKELDNSSYFRATCNDTGQFSQTHNKCRCRDKDKGANAGKPKAGDGDVTIVP 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   259 TVWGAMTCSKELDNSSYFRATCNDTGQFSQTHNKCRCRDKDKGANAGKPKAGDGDVTIVP 318

Qy   241 TYFDYVPQYLRWFEBWAEDFCRKKKKCLENLEKQCRGRDKDSDEYRYCSRNGYDCEQTISR 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   319 TYFDYVPQYLRWFEEWAEDFCRKKKKCLENLEKQCRGRDKDSDEYRYCSRNGYDCEQTISR 378

Qy   301 KGKVRMGKGCCTDCFFACGSYENWIDNQRKQFDKQKKY 337
            |||||||||||||||||||||||||||||||||||||
Db   379 KGKVRMGKGCCTDCFFACHSYENWIDNQRKQFDKQKKY 415

RESULT 2
B71600
variant-specific surface protein 1 homolog PFB1055c - malaria parasite (Plasmodium falc
N;Alternate names: erythrocyte membrane binding protein 1 (EMP1)

OM protein - protein search, using sw model

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Run on: April 26, 2005, 17:50:51 ; Search time 35.9617 Seconds
                   (without alignments)
                   3624.358 Million cell updates/sec

Title: US-09-508-967-1_COPY_79_415
Perfect score: 1884
Sequence: 1 PCKKDGKGNDVDRFSVKEQA..........GSYENWIDNQRKQFDKQKKY 337

Scoring table: BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq.16Dec04:*
         1:   geneseqp1980s:*
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         3:   geneseqp2000s:*
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         6:   geneseqp2003as:*
         7:   geneseqp2003bs:*
         8:   geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1884	100.0	2228	2	AAW93944	P. falcip
2	894	47.5	2197	3	AAB18352	Plasmodiu
3	892.5	47.4	2182	3	AAW22476	Plasmodiu
4	892.5	47.4	2182	3	AAY77906	Plasmodiu
5	885	47.0	2703	2	AAR70236	P. falcip
6	885	47.0	2710	3	AAW22482	Plasmodiu
7	885	47.0	2710	3	AAY77904	P. falcip
8	885	47.0	3060	2	AAW22475	Plasmodiu
9	885	47.0	3060	3	AAY77905	Plasmodiu
10	868.5	46.1	1700	3	AAB18144	Plasmodiu
11	861	45.7	1726	2	AAW00385	Truncated
12	861	45.7	2913	2	AAW00384	Plasmodiu
13	845	44.9	700	2	AAR70235	P. falcip
14	845	44.9	700	2	AAW22481	Plasmodiu
15	845	44.9	700	3	AAY77903	P. falcip
16	789	41.9	2647	8	ADP25446	Plasmodiu
17	653	34.7	3542	4	AAB62142	P. falcip
18	626	33.2	2459	8	ADO69969	Plasmodiu
19	624	33.1	302	8	ADO69970	Plasmodiu
20	416.5	22.1	3056	8	ADR43499	CSA-bindi
21	382.5	20.3	301	8	ADO69973	Plasmodiu
22	379.5	20.1	362	3	AAY77912	Plasmodiu
23	370.5	19.7	266	8	ADO69971	Plasmodiu
24	360.5	19.1	411	8	AAY77913	Plasmodiu
25	308.5	16.4	1143	5	AAU76759	Plasmodiu
26	308.5	16.4	1210	6	ABG73547	P. falcip
27	284.5	15.1	572	8	ADR43693	CSA-bindi
28	281	14.9	350	5	ABB07656	P. falcip
29	281	14.9	1435	2	AAR70232	P. falcip
30	281	14.9	1435	2	AAW22477	Silaic ac
31	281	14.9	1435	3	AAY77900	P. falcip
32	281	14.9	1604	2	AAR70105	P. falcip
33	281	14.9	1786	2	AAR41043	TNF-R-BBA
34	280.5	14.9	749	2	AAR70233	CD4-EBA17
35	280.5	14.9	749	2	AAW22479	P. falcip
36	280.5	14.9	749	3	AAY77901	Plasmodiu
37	280.5	14.9	1086	3	AAU76760	P. falcip
38	278	14.8	557	8	ADR43694	Plasmodiu
39	270	14.3	616	8	ABR82499	CSA-bindi
40	269	14.3	616	6	ABR82498	Synthetic
41	269	14.3	1421	5	AAU76764	Synthetic
42	267	14.2	616	5	AAM50533	Plasmodiu
43	241	12.8	793	2	AAR70234	Unidentif
44	241	12.8	921	2	AAW22480	P. falcip
45	241	12.8	921	3	AAY77902	P. falcip

ALIGNMENTS

RESULT 1
AAW93944
ID   AAW93944 standard; protein; 2228 AA.
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AC   AAW93944;
XX
DT   30-JUN-1999 (first entry)
XX
DE   P. falciparum PfEMP1 protein.
XX
KW   Erythrocyte membrane protein; EMP; PfEMP1; malaria; antiocclusional;
KW   glycosamino-glycan-like moiety; antiaggregational; antimalarial;
KW   antigen receptor; infected erythrocyte; rosette formation; blood cell;
KW   capillary occlusion; cerebral malaria; treatment; vaccine; detection;
KW   medicament; parasite; diagnosis; drug screening.
XX
OS   Plasmodium falciparum.
XX
PN   WO9915557-A1.
XX
PD   01-APR-1999.
XX
PF   18-SEP-1998;   98WO-SE001675.
XX
PR   19-SEP-1997;   97SE-00003386.
XX
PA   (KARO-) KAROLINSKA INNOVATIONS AB.
XX
PI   Wahlgren M, Barragan A, Carlson J, Qijun C, Fernandez V;
XX
DR   WPI; 1999-254692/21.
XX
PT   New isolated malaria polypeptides.
XX
PS   Claim 4; Page 67-74; 80pp; English.
XX
CC   This invention describes a novel plasmodium falciparum erythrocyte
CC   membrane protein (EMP), PfEMP1, which is capable of binding to a
CC   carbohydrate which exhibits at least one negatively charged glycosamino-
CC   glycan (GAG)-like moiety and has antiaggregational, antiocclusional and
CC   antimalarial activity. The carbohydrates of the invention are capable of
CC   acting as receptors for malaria antigens present on the surfaces of
CC   malaria infected erythrocytes, by binding to these antigens the
CC   carbohydrates prevent rosette formation by the blood cells, this prevents
CC   occlusion of capillaries as is seen in cerebral malaria caused by
CC   Plasmodium falciparum. The products of the invention can be used to treat
CC   malaria or to vaccinate against it, or used to design a model to identify
CC   compounds that bind to PfEMP1. The carbohydrates, polypeptides and

OM protein - protein search, using sw model

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Run on: April 26, 2005, 18:03:03 ; Search time 38.7148 Seconds
(without alignments)
3567.329 Million cell updates/sec

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Title:           US-09-508-967-1_COPY_1_415
Perfect score:   2276
Sequence:        1 MATSGGSSGGTQDEDAKHVLD.........GSYENWIDNQRKQFDKQKKY 415

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters:   1424015

Post-processing: Minimum Match 0%
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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database :       Published Applications AA:*
                 Listing first 45 summaries

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3:  /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
4:  /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
5:  /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
6:  /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7:  /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8:  /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9:  /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	956	42.0	2710	13	US-10-153-273-12	Sequence 12, Appl
2	845	37.1	700	13	US-10-153-273-10	Sequence 10, Appl
3	690	30.3	3542	15	US-10-087-013-2	Sequence 2, Appli
4	379.5	16.7	362	13	US-10-153-273-8	Sequence 18, Appl
5	360.5	15.8	411	13	US-10-153-273-19	Sequence 19, Appl
6	318	14.0	1143	9	US-09-924-154-14	Sequence 4, Appl
7	304	13.4	1435	13	US-10-153-273-4	Sequence 4, Appl
8	293	12.9	616	15	US-10-293-913A-4	Sequence 2, Appl
9	292	12.8	616	15	US-10-293-913A-2	Sequence 2, Appli
10	292	12.8	1421	9	US-09-924-154-13	Sequence 13, Appl
11	285.5	12.5	749	13	US-10-153-273-6	Sequence 6, Appl
12	285.5	12.5	1086	9	US-09-924-154-15	Sequence 15, Appli
13	241	10.6	921	13	US-09-153-273-8	Sequence 8, Appli
14	239	10.5	1115	13	US-10-153-273-2	Sequence 2, Appli
15	238	10.5	972	9	US-09-924-154-16	Sequence 16, Appl
16	233	10.2	407	15	US-10-087-013-8	Sequence 8, Appli
17	229.5	10.1	311	15	US-10-087-013-10	Sequence 10, Appl
18	218	9.6	308	15	US-10-087-013-11	Sequence 11, Appl
19	216.5	9.5	351	15	US-10-087-013-9	Sequence 9, Appli
20	216.5	9.5	1501	9	US-09-924-154-17	Sequence 17, Appl
21	216.5	9.5	1568	17	US-10-712-533A-12	Sequence 12, Appl
22	207	9.1	294	15	US-10-087-013-7	Sequence 7, Appli
23	197.5	8.7	411	13	US-10-153-273-16	Sequence 16, Appl
24	159.5	7.0	282	13	US-10-153-273-15	Sequence 15, Appl
25	158.5	7.0	277	13	US-10-153-273-20	Sequence 20, App
26	130.5	5.7	448	14	US-10-424-599-145507	Sequence 370, App
27	126	5.5	291	13	US-10-153-273-13	Sequence 13, Appl
28	124	5.4	706	15	US-10-104-047-3843	Sequence 3843, Ap
29	121	5.3	311	13	US-10-153-273-21	Sequence 21, Appl
30	119.5	5.3	754	14	US-10-408-765A-1486	Sequence 1486, Ap
31	116.5	5.1	1257	16	US-10-437-963-152106	Sequence 152106,
32	115.5	5.1	281	16	US-10-437-963-145507	Sequence 145507,
33	115.5	5.1	905	16	US-10-437-963-152106	Sequence 152106,
34	115	5.1	324	13	US-10-153-273-17	Sequence 17, Appl
35	114.5	5.0	610	9	US-09-989-920-212	Sequence 212, App
36	114.5	5.0	665	10	US-09-820-843A-107	Sequence 107, App
37	112.5	4.9	1737	16	US-10-437-963-194264	Sequence 194264,
38	112	4.9	1080	16	US-10-437-963-196386	Sequence 196386,
39	111	4.9	400	16	US-10-437-963-111221	Sequence 111221,
40	110.5	4.9	703	16	US-10-437-963-201481	Sequence 201481,
41	110.5	4.9	1064	14	US-10-220-510-1	Sequence 1, Appl
42	110	4.8	475	15	US-10-221-625-73	Sequence 73, Appl
43	110	4.8	933	15	US-10-369-493-12831	Sequence 12831, A
44	110	4.8	1903	16	US-10-766-993-3	Sequence 3, Appli
45	109.5	4.8	648	15	US-10-094-749-2472	Sequence 2472, Ap

ALIGNMENTS

RESULT 1
US-10-153-273-12
Sequence 12, Application US/10153273
Publication No. US20020169305A1
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
Chitnis, Chetan
Miller, Louis H.
Peterson, David S.
Su, Xin-zhuan
Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,273
FILING DATE: 21-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516

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OM protein - protein search, using sw model

Run on: April 26, 2005, 17:50:53 ; Search time 11.2802 seconds
(without alignments)
2746.348 Million cell updates/sec

Title: US-09-508-967-1_COPY_1_415
Perfect score: 2276
Sequence: 1 MATSGGSGSGTQDEDAKHVLD.........GSYENWIDNQRKQFDKQKKY 415

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents AA:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1010	44.4	2182	2	US-08-487-826B-16	Sequence 16, Appl
2	956	42.0	2710	2	US-08-568-459A-12	Sequence 12, Appl
3	956	42.0	2710	2	US-08-487-826B-12	Sequence 12, Appl
4	956	42.0	3060	3	US-09-210-288-12	Sequence 12, Appl
5	845	37.1	700	2	US-08-487-826B-14	Sequence 14, Appl
6	845	37.1	700	2	US-08-568-459A-14	Sequence 14, Appl
7	845	37.1	700	2	US-09-210-288-10	Sequence 10, Appl
8	845	37.1	700	2	US-08-487-826B-10	Sequence 10, Appl
9	379.5	16.7	362	2	US-08-568-459A-18	Sequence 18, Appl
10	379.5	16.7	362	2	US-08-487-826B-30	Sequence 30, Appl
11	379.5	16.7	362	2	US-09-210-288-18	Sequence 18, Appl
12	360.5	15.8	411	2	US-08-568-459A-19	Sequence 19, Appl
13	360.5	15.8	411	2	US-08-487-826B-31	Sequence 31, Appl
14	360.5	15.8	411	2	US-09-210-288-19	Sequence 19, Appl
15	304	13.4	1435	2	US-08-568-459A-4	Sequence 4, Appl
16	304	13.4	1435	2	US-08-487-826B-4	Sequence 4, Appl
17	304	13.4	1435	2	US-09-210-288-4	Sequence 4, Appl
18	285.5	12.5	749	2	US-08-568-459A-6	Sequence 6, Appl
19	285.5	12.5	749	2	US-08-487-826B-6	Sequence 6, Appl
20	285.5	12.5	749	2	US-09-210-288-6	Sequence 6, Appl
21	241	10.6	921	2	US-08-568-459A-8	Sequence 8, Appl
22	241	10.6	921	2	US-08-487-826B-8	Sequence 8, Appl
23	241	10.6	921	2	US-09-210-288-8	Sequence 8, Appl
24	239	10.5	1115	2	US-09-210-288-2	Sequence 2, Appl
25	239	10.5	1115	2	US-08-487-826B-2	Sequence 2, Appl
26	239	10.5	1115	3	US-09-210-288-2	Sequence 2, Appl
27	239	10.5	1115	6	5198347-6	Patent No. 5198347
28	239	10.5	1115	6	5198347-6	Patent No. 5198347
29	197.5	8.7	411	2	US-08-568-459A-20	Sequence 20, Appl
30	197.5	8.7	411	2	US-08-487-826B-32	Sequence 32, Appl
31	197.5	8.7	411	2	US-09-210-288-20	Sequence 20, Appl
32	159.5	7.0	282	2	US-08-568-459A-16	Sequence 16, Appl
33	159.5	7.0	282	2	US-08-487-826B-28	Sequence 28, Appl
34	159.5	7.0	282	2	US-09-210-288-16	Sequence 16, Appl
35	158.5	7.0	277	2	US-08-568-459A-15	Sequence 15, Appl
36	158.5	7.0	277	2	US-08-487-826B-27	Sequence 27, Appl
37	158.5	7.0	277	3	US-09-210-288-15	Sequence 15, Appl
38	150	6.6	197	3	US-08-568-459A-13	Sequence 13, Appl
39	150	6.6	197	6	US-08-487-826B-25	Sequence 25, Appl
40	150	6.6	778	6	US-09-210-288-13	Sequence 13, Appl
41	150	6.6	778	6	US-08-487-826B-25	Sequence 25, Appl
42	126	5.5	291	2	US-09-210-288-13	Sequence 13, Appl
43	126	5.5	291	3	US-08-487-826B-25	Sequence 25, Appl
44	126	5.5	291	3	US-09-210-288-13	Sequence 13, Appl
45	122.5	5.4	754	4	US-09-976-594-375	Sequence 375, App

ALIGNMENTS

RESULT 1
US-08-487-826B-16
Sequence 16, Application US/08487826B
Patent No. 5993827
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhuan
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2182 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-487-826B-16

Query Match   44.4%;   Score 1010;   DB 2;   Length 2182;

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                    GenCore version 5.1.6
            Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw_model

Run on:     April 26, 2005, 17:50:52 ; Search time 50.4128 Seconds
                                        (without alignments)
                                        4215.459 Million cell updates/sec

Title:        US-09-508-967-1_COPY_1_415
Perfect Score: 2276
Sequence:     1 MATSGGSGGGTQDEDAKHVLD..........GSYENWIDNQRKKQFDKQKKY 415

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:     1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:        1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  UniProt_03:*
            1: uniprot_sprot:*
            2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	Match DB	ID	Description
1	2268	99.6	2228	2	O60991	O60991 plasmodium
2	1344	59.1	2275	2	Q81bx2	Q81bx2 plasmodium
3	1253.5	55.1	2215	2	Q81bx3	Q81bx3 plasmodium
4	1224	53.8	2209	2	Q9U0G6	Q9U0G6 plasmodium
5	1203.5	52.9	2215	2	Q81BW9	Q81BW9 plasmodium
6	1139	50.0	2326	2	Q81iv6	Q81iv6 plasmodium
7	1139	50.0	2152	2	Q81fq6	Q81fq6 plasmodium
8	1137.5	50.0	2201	2	Q81fq5	Q81fq5 plasmodium
9	1134	49.8	2267	2	Q81bx1	Q81bx1 plasmodium
10	1114.5	49.0	2149	2	Q81fk7	Q81fk7 plasmodium
11	1108.5	48.7	2264	2	Q812e3	Q812e3 plasmodium
12	1104	48.5	2192	2	Q81bw7	Q81bw7 plasmodium
13	1057	46.4	2193	2	Q81fq2	Q81fq2 plasmodium
14	1049	46.1	2231	2	Q81as4	Q81as4 plasmodium
15	1038.5	45.6	2162	2	Q81ev1	Q81ev1 plasmodium
16	1038.5	45.6	2207	2	Q81495	Q81495 plasmodium
17	1036	45.5	2199	2	Q96296	Q96296 plasmodium
18	1031	45.3	2277	2	Q9U0G5	Q9U0G5 plasmodium
19	1031	45.3	2312	2	Q81iv7	Q81iv7 plasmodium
20	1024	45.0	2710	2	Q9XZB8	Q9XZB8 plasmodium
21	1015	44.6	2359	2	Q81519	Q81519 plasmodium
22	1010	44.4	2182	2	Q26034	Q26034 plasmodium
23	1004	44.1	2265	2	Q81a83	Q81a83 plasmodium
24	1003.5	44.1	2223	2	Q81d12	Q81d12 plasmodium
25	994.5	43.7	2646	2	Q81220	Q81220 plasmodium
26	993.5	43.7	3954	2	Q61ev2	Q61ev2 plasmodium
27	983.5	43.2	3026	2	Q26030	Q26030 plasmodium
28	980	43.1	1729	2	Q25734	Q25734 plasmodium
29	980	43.1	2924	2	Q25733	Q25733 plasmodium
30	979	43.0	2182	2	Q81i25	Q81i25 plasmodium
31	978.5	43.0	2241	2	Q81k37	Q81k37 plasmodium
32	965.5	42.4	2135	2	061077	061077 plasmodium
33	961.5	42.2	2256	2	Q81515	Q81515 plasmodium
34	957	42.1	1711	2	096108	096108 plasmodium
35	956	42.0	3078	2	026031	026031 plasmodium
36	952	41.8	2268	2	Q814N5	Q814N5 plasmodium
37	951.5	41.8	2270	2	Q813E5	Q813E5 plasmodium
38	947	41.6	2287	2	Q81520	Q81520 plasmodium
39	934.5	41.1	2163	2	Q9NFB6	Q9NFB6 plasmodium
40	917.5	40.3	2239	2	Q81BD8	Q81BD8 plasmodium
41	907	39.9	2595	2	Q81BW8	Q81BW8 plasmodium
42	893.5	39.5	2169	2	Q97312	Q97312 plasmodium
43	893.5	39.3	2109	2	Q81A87	Q81A87 plasmodium
44	888	39.0	2181	2	Q81FQ4	Q81FQ4 plasmodium
45	882.5	38.8	2209	2	097324	097324 plasmodium

ALIGNMENTS

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RESULT 1
O60991

ID   O60991     PRELIMINARY;    PRT;   2228 AA.
AC   O60991;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Erythrocyte membrane protein 1.
GN   Name=PCR3S1.2-var1;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98080592; PubMed=9419207;
RA   Chen Q.J., Wahlgren M.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Chen Q., Barragan A., Fernandez V., Sundstrom A., Schlichtherle M.,
RA   Sahlen A., Carlson J., Datta S., Wahlgren M.;
RT   "Identification of Plasmodium falciparum erythrocyte membrane protein
RT   1 (PfEMP1) as the rosetting ligand of the malaria parasite P.
RT   falciparum.";
RL   J. Exp. Med. 187:15-23(1998).
DR   EMBL; AF003473; AAC05730.1; -.
DR   PIR; T14029; T14029.
DR   GO; GO:0005539; P:glycosaminoglycan binding; IEA.
DR   GO; GO:0009405; P:pathogenesis; IEA.
DR   InterPro; IPR004258; PfEMP.
DR   Pfam; PF03011; PfEMP; 2.
SQ   SEQUENCE   2228 AA;  5D8C8E9BPA22DC8B CRC64;

Query Match         99.6%;  Score 2268;  DB 2;  Length 2228;
Best Local Similarity  99.8%;
Matches  414;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;
                            Pred. No. 6.7e-144;

Qy      1 MATSGGSGGGTQDEDAKHVLDEFGQKVHDEVHGEAKNVVSELKGSLSLASILGETAFTVKS 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MATSGGSGGGTQDEDAKHVLDEFGQKVHDEVHGEAKNVVSELKGSLSLASILGETAFTVKS 60

Qy     61 MQTESKYTELIEANSKRNPCKKDGKGNDVDRFSVKEQAGYDNKQMKCSNGMTCAPFRRLH 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MQTESKYTELIEANSKRNPCKKDGKGNDVDRFSVKEQAGYDNKQMKCSNGMTCAPFRRLH 120

Qy    121 LCNKNFPNMSNDSSKAKHDLLAEVCMAAKYEGESIKTHYPKYDSKYFPGSDFPMCTMLAR 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 LCNKNFPNMSNDSSKAKHDLLAEVCMAAKYEGESIKTHYPKYDSKYFPGSDFPMCTMLAR 180

Qy    181 SFADIGDIIRGRDLYLGNKKKKQNGKETERRKLEQKLKEIFKKIHDNLKDKEAQKRYNGD 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 SFADIGDIIRGRDLYLGNKKKKQNGKETERRKLEQKLKEIFKKIHDNLKDKEAQKRYNGD 240

Qy    241 EDPNFYKGREDWWTANRETVWGAMTCSKELDNSSYPRATCNDTGQGPSQTHNKCRCDKDK 300
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OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: April 26, 2005, 17:50:53 ; Search time 8.07718 Seconds
(without alignments)
4943.551 Million cell updates/sec

Title: US-09-508-967-1_COPY_1_415
Perfect score: 2276
Sequence: 1 MATSGGGSGGTQDEDAKHVLD...........GSYENWIDNQRKQFDKQKKY 415
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Database : PIR.79:*
1: pir1:*
2: pir1:*
3: pir3:*
4: pir4:*

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Maximum DB seq length: 2000000000
Minimum DB seq length: 0

Total number of hits satisfying chosen parameters: 283416

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2268	99.6	2228	2	T14029	variant-specific s
2	1036	45.5	2197	2	B71600	variant-specific s
3	1010	44.4	2182	2	T28634	variant-specific s
4	983.5	43.2	3026	2	T28431	variant surface pr
5	980	43.1	1729	2	T18396	erythrocyte membra
6	980	43.1	2924	2	T18378	variant-specific s
7	965.5	42.4	2135	2	T14602	variant-specific s
8	957	42.0	1711	2	C71625	variant-specific s
9	956	42.0	3078	2	T28432	variant-specific s
10	871.5	38.3	2647	2	T28161	hypothetical prote
11	864.5	38.0	2664	2	T28626	variant-specific s
12	857.5	37.7	2212	2	T28157	erythrocyte membra
13	791.5	34.8	3006	2	T28625	variant-specific s
14	680	29.9	2042	2	T18399	variant-specific s
15	666.5	29.3	2706	2	T18155	variant-specific s
16	304	13.4	1435	2	A37793	erythrocyte-bindin
17	239	10.5	1070	2	T30848	Duffy receptor - P
18	214	9.4	1045	2	T18373	erythrocyte bindin
19	194	8.5	1153	2	T28652	erythrocyte bindin
20	150	6.6	778	2	A35970	erythrocyte-bindin
21	125	5.5	1979	2	C71622	hypothetical prote
22	119.5	5.3	754	1	JC5314	CDC28/cdc2-like ki
23	119	5.3	590	2	A25680	nuclear histone-bi
24	119	5.2	2441	2	D71623	erythrocyte membra
25	118	5.2	715	2	JC2222	major surface glyc
26	118	5.2	929	2	T29162	hypothetical prote
27	118	5.2	4550	2	T18440	hypothetical prote
28	117	5.1	807	2	T18454	hypothetical prote
29	116.5	5.1	1257	1	I58383	retinoblastoma bin
30	116	5.1	1076	2	C70007	hypothetical prote
31	116	5.1	1390	2	S51364	sperm tail-specifi
32	115	5.1	1282	2	JB0120	glycoprotein A - m
33	115	5.1	2523	2	T18477	hypothetical prote
34	114.5	5.0	665	2	B71609	hypothetical prote
35	113.5	5.0	2116	2	A26655	myosin heavy chain
36	112	4.9	710	2	I48668	zinc finger protei
37	111	4.9	522	2	C96608	hypothetical prote
38	111	4.9	426	2	G36891	transfer complex p
39	111	4.9	911	2	T13216	hypothetical prote
40	111	4.9	1608	2	S41649	DNA polymerase - m
41	111	4.9	1855	2	S51441	minor capsid prote
42	110.5	4.9	980	2	E71606	hypothetical prote
43	110.5	4.9	990	2	E71620	hypothetical prote
44	109.5	4.8	1002	2	T30546	major surface glyc
45	109	4.8	508	2	H88733	protein F32E10.3 [

ALIGNMENTS

RESULT 1
T14029
variant-specific surface protein; erythrocyte membrane binding protein 1 (Plasmodium falciparum)
N;Alternate names: erythrocyte membrane binding protein 1 (EMP1)
A;Title: Identification of Plasmodium falciparum erythrocyte membrane protein 1 (PfEMP1
A;Reference number: Z17860; MUID:98080592; PMID:9419207
A;Accession: T14029
C;Species: Plasmodium falciparum
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
R;Chen, Q.; Barragan, A.; Fernandez, V.; Sundstrom, A.; Schlichtherle, M.; Sahlen, A.;
J. Exp. Med. 187, 15-23, 1998
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2228 <CHE>
A;Cross-references: UNIPROT:O60991; EMBL:AF003473; NID:g2961467; PID:g2961468; PIDN:AAC
C;Genetics:
A;Note: FCR3S1.2-var1

Query Match 99.6%; Score 2268; DB 2; Length 2228;
Best Local Similarity 99.8%;
Matches 414; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy    1 MATSGGGSGGTQDEDAKHVLDEFGQKVHDEVHGEAKQNYVSELKGSLSLASILGETAPTVKSS  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    1 MATSGGGSGGTQDEDAKHVLDEFGQKVHDEVHGEAKQNYVSELKGSLSLASILGETAPTVKS   60

Qy   61 MQTESKYTELIEANSKRNPCKKDGKGNDVDRFSVKEQAGYDNKKMKCSNGMTCAPFRRLH  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 MQTESKYTELIEANSKRNPCKKDGKGNDVDRFSVKEQAGYDNKKMKCSNGMTCAPFRRLH  120

Qy  121 LCNKNFPNMNSNDSSKAKHDLLAEVCMAAKYEGESIKTHYPKYDSKYPGSDFPMCTMLAR  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 LCNKNFPNMNSNDSSKAKHDLLAEVCMAAKYEGESIKTHYPKYDSKYPGSDFPMCTMLAR  180

Qy  181 SFADIGDIIRGRDLYLGNKKCKKQNGKETEREKLEQKLKEIFKKIHDNLKDKEAQRYNGD  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 SFADIGDIIRGRDLYLGNKKCKKQNGKETEREKLEQKLKEIFKKIHDNLKDKEAQRYNGD  240

Qy  241 EDPNFYKLREDWWTANRETVWGAMTCSKELDNSSYFRATCNDTGQGPSQTHNKCRCDKDK  300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 EDPNFYKLREDWWTANRETVWGAMTCSKELDNSSYFRATCNDTGQGPSQTHNKCRCDKDK  300

Qy  301 GANAGKPKAGDGDVTIVPTYFDYVPQYLRWFEEWAEDFCRKKKKKLENLEKQCRGKDKSD  360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 GANAGKPKAGDGDVTIVPTYFDYVPQYLRWFEEWAEDFCRKKKKKLENLEKQCRGKDKSD  360

Qy  361 EYRYCSRNGYDCEQTISRKGKVRMGKGCTDCFPACGSYENWIDNQRKQFDKQKKY  415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 EYRYCSRNGYDCEQTISRKGKVRMGKGCTDCFPACGSYENWIDNQRKQFDKQKKY  415
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                    GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:          April 26, 2005, 17:50:51 ; Search time 44.2852 Seconds
                                           (without alignments)
                                           3624.358 Million cell updates/sec

Title:           US-09-508-967-1_COPY_1_415
Perfect Score:   2276
Sequence:        1 MATSGGSGSGGTQDEDAKHVLD............GSYENWIDNQRKQFDKQKKY 415
Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5
Searched:        2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters:      2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Databases :      A Geneseq_16Dec04:*
             1:  geneseqp1980s:*
             2:  geneseqp1990s:*
             3:  geneseqp2000s:*
             4:  geneseqp2001s:*
             5:  geneseqp2002s:*
             6:  geneseqp2003as:*
             7:  geneseqp2003bs:*
             8:  geneseqp2004s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID		Description
1	2276	100.0	2228	2	AAW93944	Aaw93944	P. falcip
2	1036	45.5	2197	2	AAB18352	Aab18352	Plasmodiu
3	1010	44.4	2182	2	AAW22476	Aaw22476	Plasmodiu
4	1010	44.4	2182	3	AAY77906	Aay77906	Plasmodiu
5	972	42.7	1726	2	AAW00385	Aaw00385	Truncated
6	972	42.7	2913	2	AAW00384	Aaw00384	Plasmodiu
7	957	42.0	1700	3	AAB18144	Aab18144	Plasmodiu
8	956	42.0	2703	2	AAR70236	Aar70236	P. falcip
9	956	42.0	2710	2	AAW22482	Aaw22482	Plasmodiu
10	956	42.0	2710	3	AAY77904	Aay77904	P. falcip
11	956	42.0	3060	2	AAW22475	Aaw22475	Plasmodiu
12	956	42.0	3060	3	AAY77905	Aay77905	Plasmodiu
13	871.5	38.3	2647	8	ADP25446	Adp25446	Plasmodiu
14	845	37.1	700	2	AAR70235	Aar70235	P. falcip
15	845	37.1	700	2	AAW22481	Aaw22481	Plasmodiu
16	845	37.1	700	3	AAY77903	Aay77903	P. falcip
17	690	30.3	3542	4	AAB62142	Aab62142	P. falcip
18	676	29.7	2459	8	AD069969	Ado69969	Plasmodiu
19	624	27.4	302	8	AD069970	Ado69970	Plasmodiu
20	421	18.5	3056	8	ADR43499	Adr43499	CSA-bindi
21	382.5	16.8	3056	8	AD069973	Ado69973	Plasmodiu
22	379.5	16.7	362	3	AAY77912	Aay77912	Plasmodiu
23	370.5	16.3	266	8	AD069971	Ado69971	Plasmodiu
24	360.5	15.8	411	3	AAY77913	Aay77913	Plasmodiu
25	318	14.0	1143	5	AAU76759	Aau76759	Plasmodiu
26	318	14.0	1210	6	ABG73547	Abg73547	P. falcip
27	304	13.4	1435	2	AAR70232	Aar70232	P. falcip
28	304	13.4	1435	2	AAW22477	Aaw22477	Silaic ac
29	304	13.4	1435	3	AAY77900	Aay77900	P. falcip
30	304	13.4	1604	2	AAR70105	Aar70105	TNF-R-EBA
31	304	13.4	1786	2	AAR41043	Aar41043	CD4-EBA17
32	293	12.9	616	6	ABR82499	Abr82499	Synthetic
33	292	12.8	616	6	ABR82498	Abr82498	Synthetic
34	292	12.8	1421	5	AAU76764	Aau76764	Plasmodiu
35	290	12.7	616	5	AAM50533	Aam50533	Unidentif
36	286.5	12.6	572	8	ADR43693	Adr43693	CSA-bindi
37	285.5	12.5	749	2	AAR70233	Aar70233	P. falcip
38	285.5	12.5	749	2	AAW22479	Aaw22479	Plasmodiu
39	285.5	12.5	749	3	AAY77901	Aay77901	P. falcip
40	285.5	12.5	1086	5	AAU76760	Aau76760	Plasmodiu
41	281	12.3	350	5	ABB07656	Abb07656	P. falcip
42	280	12.3	557	8	ADR43694	Adr43694	CSA-bindi
43	249.5	11.0	1245	5	AAR70106	Aar70106	TNF-R-Pl.
44	241	10.6	793	2	AAR70234	Aar70234	P. falcip
45	241	10.6	921	2	AAW22480	Aaw22480	Plasmodiu

ALIGNMENTS

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ID   AAW93944 standard; protein; 2228 AA.
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AC   AAW93944;
XX
DT   30-JUN-1999  (first entry)
XX
DE   P. falciparum PfEMP1 protein.
XX
KW   Erythrocyte membrane protein; EMP; PfEMP1; malaria; antiocclusional;
KW   glycosamino-glycan-like moiety; antiaggregational; antimalarial;
KW   antigen receptor; infected erythrocyte; rosette formation; blood cell;
KW   capillary occlusion; cerebral malaria; treatment; vaccine; detection;
KW   medicament; parasite; diagnosis; drug screening.
XX
OS   Plasmodium falciparum.
XX
PN   WO9915557-A1.
XX
PD   01-APR-1999.
XX
PF   18-SEP-1998;  98WO-SE001675.
XX
PR   19-SEP-1997;  97SE-00003386.
XX
PA   (KARO-) KAROLINSKA INNOVATIONS AB.
XX
PI   Wahlgren M, Barragan A, Carlson J, Qijun C, Fernandez V;
XX
DR   WPI; 1999-254692/21.
XX
PT   New isolated malaria polypeptides.
XX
PS   Claim 4; Page 67-74; 80pp; English.
XX
CC   This invention describes a novel Plasmodium falciparum erythrocyte
CC   membrane protein (EMP), PfEMP1, which is capable of binding to a
CC   carbohydrate which exhibits at least one negatively charged glycosamino-
CC   glycan (GAG)-like moiety and has antiaggregational, antiocclusional and
CC   antimalarial activity. The carbohydrates of the invention are capable of
CC   acting as receptors for malaria antigens present on the surfaces of
CC   malaria infected erythrocytes, by binding to these antigens the
CC   carbohydrates prevent rosette formation by the blood cells, this prevents
CC   occlusion of capillaries as is seen in cerebral malaria caused by
CC   Plasmodium falciparum. The products of the invention can be used to treat
CC   malaria or to vaccinate against it, or used to design a model to identify
CC   compounds that bind to PfEMP1. The carbohydrates, polypeptides and
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OM protein - protein search, using sw model
                    GenCore version 5.1.6
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Run on:          April 26, 2005, 18:03:03 ; Search time 207.847 Seconds
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Title:           US-09-508-967-1
Perfect score:   12100
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                 Gapop 10.0 , Gapext 0.5
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Total number of hits satisfying chosen parameters:    1424015

Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	702	5.8	921	13	US-10-153-273-8	Sequence 8, Appli
5	445	3.7	311	15	US-10-087-013-10	Sequence 10, Appl
6	439.5	3.6	407	15	US-10-087-013-8	Sequence 8, Appl
7	422	3.5	294	15	US-10-087-013-7	Sequence 7, Appli
8	421.5	3.5	1421	9	US-09-924-154-13	Sequence 13, Appli
9	418	3.5	1435	13	US-10-153-273-4	Sequence 4, Appli
10	396	3.3	1086	9	US-09-924-154-15	Sequence 15, Appli
11	386	3.2	308	15	US-10-087-013-11	Sequence 11, Appl
12	379.5	3.1	362	13	US-10-153-273-18	Sequence 18, Appl
13	376	3.1	1501	9	US-09-924-154-17	Sequence 17, Appl
14	376	3.1	1568	17	US-10-712-533A-12	Sequence 12, Appl
15	375	3.1	351	15	US-10-087-013-9	Sequence 9, Appl
16	371.5	3.1	1143	9	US-09-924-154-14	Sequence 14, Appl
17	360.5	3.0	411	13	US-10-153-273-19	Sequence 19, Appl
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23	284	2.3	6642	15	US-10-369-493-5013	Sequence 5013, Ap
24	282.5	2.3	3507	15	US-10-369-493-5784	Sequence 5784, Ap
25	273	2.3	10203	15	US-10-661-809-23	Sequence 23, Appl
26	271	2.2	6641	15	US-10-282-122A-70580	Sequence 70580, A
27	266.5	2.2	2492	16	US-10-697-526-2	Sequence 2, Appli
28	265.5	2.2	1639	14	US-10-087-464-10	Sequence 10, Appl
29	263	2.2	3692	15	US-10-282-122A-71235	Sequence 71235, A
30	259.5	2.1	2052	15	US-10-282-122A-51602	Sequence 51602, A
31	259	2.1	972	9	US-09-924-154-16	Sequence 16, Appl
32	258	2.1	3225	16	US-10-408-765A-254	Sequence 254, App
33	257.5	2.1	5560	15	US-10-263-929-142	Sequence 142, App
34	254.5	2.1	2785	9	US-09-801-574-8	Sequence 8, Appl.
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36	251.5	2.1	2476	15	US-09-824-574-7	Sequence 7, Appli
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42	245	2.0	2375	16	US-10-408-765A-277	Sequence 277, App
43	243.5	2.0	2058	16	US-10-052-648A-20	Sequence 20, Appl
44	242.5	2.0	2481	15	US-10-282-122A-43762	Sequence 43762, A
45	239.5	2.0	4688	15	US-10-282-122A-76865	Sequence 76865, A

ALIGNMENTS

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RESULT 1
US-10-153-273-12
Sequence 12, Application US10153273
Publication No. US20020169305A1
GENERAL INFORMATION:
   APPLICANT: Sim, Kim L.
              Chitnis, Chetan
              Miller, Louis H.
              Peterson, David S.
              Su, Xin-zhuan
              Wellems, Thomas E.
   TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
            AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
   NUMBER OF SEQUENCES: 37
   CORRESPONDENCE ADDRESS:
      ADDRESSEE: Knobbe Martens Olson & Bear
      STREET: 620 Newport Center Drive 16th Floor
      CITY: Newport Beach
      STATE: California
      COUNTRY: US
      ZIP: 92660
   COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patentin Release #1.0, Version #1.25
   CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/10/153,273
      FILING DATE: 21-May-2002
      CLASSIFICATION: <Unknown>
   PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US/09/210,288
      FILING DATE: <Unknown>
   ATTORNEY/AGENT INFORMATION:
      NAME: Fuller, Michael
      REGISTRATION NUMBER: 36,516
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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: April 26, 2005, 17:50:53 ; Search time 60.5597 Seconds
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Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	3197.5	26.4	2710	3	US-09-210-288-12	Sequence 12, Appl
6	1385	11.4	700	2	US-08-568-459A-10	Sequence 10, Appl
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9	702	5.8	921	2	US-08-568-459A-8	Sequence 8, Appl
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13	418	3.5	1435	2	US-08-487-826B-4	Sequence 4, Appli
14	418	3.5	1435	3	US-09-210-288-4	Sequence 4, Appli
15	379.5	3.1	362	2	US-08-568-459A-18	Sequence 18, Appl
16	379.5	3.1	362	2	US-08-487-826B-30	Sequence 30, Appl
17	379.5	3.1	362	3	US-09-210-288-18	Sequence 18, Appl
18	360.5	3.0	411	2	US-08-568-459A-19	Sequence 19, Appl
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20	360.5	3.0	411	3	US-09-210-288-19	Sequence 19, Appl
21	345.5	2.9	749	2	US-08-568-459A-6	Sequence 6, Appl
22	345.5	2.9	749	2	US-08-487-826B-6	Sequence 6, Appl
23	345.5	2.9	749	3	US-09-210-288-6	Sequence 6, Appli
24	315	2.6	1115	2	US-08-568-459A-2	Sequence 2, Appli
25	315	2.6	1115	2	US-08-487-826B-2	Sequence 2, Appli
26	315	2.6	1115	3	US-09-210-288-2	Sequence 2, Appli
27	315	2.6	1115	6	5198347-6	Patent No. 5198347
28	315	2.6	1115	6	5198347-6	Patent No. 5198347
29	311.5	2.6	1663	5	PCT-US93-07261-16	Sequence 16, Appl
30	288	2.4	1588	5	PCT-US93-07261-11	Sequence 11, Appl
31	272.5	2.3	2907	5	US-09-698-295-1	Sequence 1, Appli
32	272	2.2	10182	3	US-09-134-001C-3159	Sequence 3159, Ap
33	267	2.2	5024	4	US-09-710-279-2964	Sequence 2964, Ap
34	265	2.2	3696	3	US-09-134-001C-5080	Sequence 5080, Ap
35	262.5	2.2	3969	3	US-09-538-092-1262	Sequence 1262, Ap
36	262.5	2.2	3969	4	US-09-949-016-6507	Sequence 6507, Ap
37	258	2.1	3259	4	US-09-538-092-914	Sequence 7, Appli
38	251.5	2.1	2476	4	US-09-824-574-7	Sequence 914, App
39	249.5	2.1	2781	4	US-09-538-092-10	Sequence 10, Appl
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ALIGNMENTS

RESULT 1
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; Sequence 16, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellems, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-0176
; TELEFAX: (619) 235-8550
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-487-826B-16

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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: April 26, 2005, 17:50:52 ; Search time 270.65 Seconds
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Title: 12100
Perfect score: 12100
Sequence: 1 MATSGGSGGTGQDEDAKHVLD.........VNNKKEIFEEEYPISDIWNI 2228

Scoring table: BLOSUM62
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Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	5220	43.1	2192	2	Q81BW9	Q81BW9 plasmodium
6	5216.5	43.1	2277	2	Q81BW7	Q81BW7 plasmodium
7	5159	42.6	2275	2	Q9U0G5	Q9U0G5 plasmodium
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13	4817	39.8	2182	2	Q26031	Q26031 plasmodium
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32	4493.5	37.1	2163	2	Q9nfb6	Q9nfb6 plasmodium
33	4464.5	36.9	2109	2	Q81A87	Q81A87 plasmodium
34	4432	36.5	2312	2	Q81V7	Q81V7 plasmodium
35	4418.5	36.5	2201	2	Q81V7	Q81V7 plasmodium
36	4381	36.2	2152	2	Q81FQ5	Q81FQ5 plasmodium
37	4346.5	35.9	2203	2	Q81FQ6	Q81FQ6 plasmodium
38	4341.5	35.9	2169	2	Q812C4	Q812C4 plasmodium
39	4310.5	35.6	2178	2	Q97312	Q97312 plasmodium
40	4302.5	35.6	2209	2	Q97324	Q97324 plasmodium
41	4285	35.4	2268	2	Q81643	Q81643 plasmodium
42	4270.5	35.3	2270	2	Q814N5	Q814N5 plasmodium
43	4268.5	35.3	2215	2	Q813E5	Q813E5 plasmodium
44	4267.5	35.3	2239	2	Q81IZ6	Q81IZ6 plasmodium
45	4210	34.8	2120	2	Q81BW8	Q81BW8 plasmodium
					Q81aK1	Q81aK1 plasmodium

ALIGNMENTS

RESULT 1
O60991
ID   O60991   PRELIMINARY;   PRT;   2228 AA.
AC   O60991;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Erythrocyte membrane protein 1.
GN   Name=PfCR3S1.2-vari;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98080592; PubMed=9419207;
RA   Chen Q.J., Wahlgren M.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Chen Q., Barragan A., Fernandez V., Sundstrom A., Schlichtherle M.,
RA   Sahlen A., Carlson J., Datta S., Wahlgren M.;
RT   "Identification of Plasmodium falciparum erythrocyte membrane protein
RT   1 (PfEMP1) as the rosetting ligand of the malaria parasite P.
RT   falciparum.";
RL   J. Exp. Med. 187:15-23(1998).
DR   EMBL; AF003473; AAC05730.1; -.
DR   PIR; T14029; T14029.
DR   GO; GO:0005539; F:glycosaminoglycan binding; IEA.
DR   GO; GO:0009405; P:pathogenesis; IEA.
DR   InterPro; IPR004258; PfEMP.
DR   Pfam; PF03011; PfEMP; 2.
SQ   SEQUENCE   2228 AA;   252811 MW;   5D8C8E9BFA22DC8B CRC64;

Query Match   99.7%;   Score 12065;   DB 2;   Length 2228;
Best Local Similarity   99.8%;   Pred. No. 0;
Matches 2223;   Conservative   0;   Mismatches   5;   Indels   0;   Gaps   0;

Qy   1 MATSGGSGGTGQDEDAKHVLDEFGQKVHDEVHGEAKNYVVSELKGSLSLASILGBTAFTVKS   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MATSGGSGGTGQDEDAKHVLDEFGQKVHDEVHGEAKNYVVSELKGSLSLASILGETAFTVKS   60

Qy   61 MQTESKYTELIEANSKRNPCKKDGKGNDVDRFSVKEQAGYDNKKMKCSNGMTCAPFRRLH 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 MQTESKYTELIEANSKRNPCKKDGKGNDVDRFSVKEQAGYDNKKMKCSNGMTCAPFRRLH 120

Qy 121 LCNKNFPNMNSNDSSKAKHDLLAEVCMAAKYEGESIKTHYPKYDSKYPGSDPPMCTMLAR 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 LCNKNFPNMNSNDSSKAKHDLLAEVCMAAKYEGESIKTHYPKYDSKYPGSDPPMCTMLAR 180

Qy 181 SFADIGDIIRGRDLYLGNKKKKQNGKETEREKCLEQKLKBIFKKIHDNLKDKBAQKRYNGD 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 SFADIGDIIRGRDLYLGNKKKKQNGKETEREKCLEQKLKEIFKKIHDNLKDKBAQKRYNGD 240

Qy 241 EDPNFYKLREDWWTANRETWGAMTCSKELDNSSYFRATCNDTGGPSQTHNKCRCDKDK 300

OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: April 26, 2005, 17:50:53 ; Search time 43.3638 Seconds
(without alignments)
4943.551 Million cell updates/sec

Title: US-09-508-967-1
Perfect score: 12100
Sequence: 1 MATSGGSGGTQDEDAKHVLD..........VNNKKEIFEBEVYPISDIWNI 2228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Maximum DB seq length: 200000000
Minimum DB seq length: 0

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first: 45 summaries

Database : PIR.79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	12065	99.7	2228	2	T14029	variant-specific surface p
2	5074	41.9	2197	2	B71600	variant-specific s
3	4901	40.5	3078	2	T28432	variant-specific s
4	4817	39.8	2182	2	T28634	variant-specific s
5	4711	38.9	2664	2	T28626	variant-specific s
6	4084	33.8	2647	2	T28161	variant-specific s
7	4073	33.7	2042	2	T18399	hypothetical prote
8	3937	33.0	3006	2	T28625	variant-specific s
9	3937	33.0	2924	2	T18378	variant-specific s
10	3297.5	27.3	1711	2	C71625	variant-specific s
11	3192	26.4	2706	2	T28155	variant-specific s
12	2959	24.5	1729	2	T18396	variant-specific s
13	2863	23.7	2212	2	T28157	erythrocyte membra
14	2668	22.0	3026	2	T28431	variant surface pr
15	2518	20.8	2135	2	T14602	variant-specific s
16	1319.5	10.9	431	2	P71600	variant-specific s
17	782	6.5	440	2	E71625	variant-specific s
18	418	3.5	1435	2	A37793	erythrocyte-bindin
19	406	3.4	248	2	C71624	variant-specific s
20	360	3.0	4550	2	T18440	hypothetical prote
21	339	2.8	1526	2	A45605	mature-parasite-in
22	329.5	2.7	3394	2	T18501	hypothetical prote
23	321.5	2.7	2523	2	D71623	hypothetical prote
24	321	2.7	2441	2	D71623	erythrocyte membra
25	318.5	2.6	2401	2	T28676	rhoptry protein
26	315	2.6	1070	2	T30848	Duffy receptor - P
27	310.5	2.6	1979	2	C71622	rhoptry protein -
28	303	2.5	2269	2	T28677	hypothetical prote
29	301	2.5	2829	2	A42771	reticulocyte-bindi
30	300.5	2.5	3724	2	T18427	hypothetical prote
31	287	2.4	1308	2	B71622	probable membrane
32	285	2.4	1871	2	D96796	probable heat shoc
33	284	2.3	6642	2	T29757	protein UNC-89 - C
34	283.5	2.3	3844	2	T18402	asparagine/asparta
35	282.5	2.3	3507	2	T34513	hypothetical prote
36	279.5	2.3	1939	2	T18372	repeat organellar
37	277.5	2.3	2485	1	S55101	serine/threonine-s
38	271	2.2	1631	1	H71621	major merozoite su
39	269.5	2.2	1658	2	SAZQK1	major merozoite su
40	267.5	2.2	1726	2	A45948	major merozoite su
41	265.5	2.2	1639	2	S05603	hypothetical prote
42	265	2.2	2657	2	T18497	hypothetical prote
43	263.5	2.2	1640	2	A24594	probable major sur
44	262.5	2.2	1045	2	T18373	erythrocyte bindin
45	262.5	2.2	1726	1	SAZQGM	major merozoite su

ALIGNMENTS

RESULT 1
T14029
variant-specific surface protein 1 - malaria parasite (Plasmodium falciparum)
N;Alternate names: erythrocyte membrane binding protein 1 (EMP1)
C;Species: Plasmodium falciparum
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14029
R;Chen, Q.; Barragan, A.; Fernandez, V.; Sundstrom, A.; Schlichtherle, M.; Sahlen, A.; C
J. Exp. Med. 187, 15-23, 1998
A;Title: Identification of Plasmodium falciparum erythrocyte membrane protein 1 (PfEMP1)
A;Reference number: Z17860; MUID:98080592; PMID:9419207
A;Accession: T14029
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2228 <CHE>
A;Cross-references: UNIPROT:O60991; EMBL:AF003473; NID:g2961467; PID:g2961468; PIDN:AAC0
A;Note: PCR3S1.2-var1

Query Match 99.7%; Score 12065; DB 2; Length 2228;
Best Local Similarity 99.8%;
Matches 2222; Conservative 0; Pred. No. 0; Mismatches 5; Indels 0; Gaps 0;

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Qy     1 MATSGGSGSGGTQDEDAKHVLDEFGQKVHDEVHGEAKNYVSELKGSLSLASILGETAFTVKS 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MATSGGSGSGGTQDEDAKHVLDEFGQKVHDEVHGEAKNYVSELKGSLSLASILGETAFTVKS 60

Qy    61 MQTESKYTELIEANSKRNPCKKDGKGNDVDRFSVKEQAGYDNKQMKCSNGMTCAPFRRLH 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 MQTESKYTELIEANSKRNPCKKDGKGNDVDRFSVKEQAGYDNKKQMKCSNGMTCAPFRRLH 120

Qy   121 LCNKNFPNMNSNDSSKAKHDLLAEVCMAAKYEGBSIKTHYPKYDSKYPGSSDFPMCTMLAR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 LCNKNFPNMNSNDSSKAKHDLLAEVCMAAKYEGSSIKTHYPKYDSKYPGSSDFPMCTMLAR 180

Qy   181 SFADIGDIIRGRDLYLGNKKCKQNGKETEREKLBQKLKEIFKKIHDNLKDKEAQKRYNGD 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 SFADIGDIIRGRDLYLGNKKCKKQONGKETEREKLBQKLKBIFKKIHDNLKDKBAQKRYNGD 240

Qy   241 EDDNFYKLREDWWTANRETVWGAMTCSKELDNSSYFRATCNDTGQPSQTHNKCRCDKDK 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 EDDNFYKLREDWWTANRETVWGAMTCSKELDNSSYFRATCNDTGQPSQTHNKCRCDKDK 300

Qy   301 GANAGKPKAGDGDVTIVPTYFDYVPQYLRWFEEWAEDFCRKKKKKCLENLEKQCRGKDKSD 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GANAGKPKAGDGDVTIVPFYFDYVPQYLRWFSEWAEDFCRKKKKCLENLEKQCRGKDKSD 360

Qy   361 EYRYCSRNGYDCEQTISRKGKVRMGKGCTDCFPACGSYENWIDNQRKQFDKQKKYTKBIS 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 EYRYCSRNGYDCEQTISRKGKVRMGKGCTDCFPACHSYENWIDNQRKQFDKQKKYTKBIS 420

Qy   421 DGGGRKKRAVGGTTKYEGYEKSFYEKLKNDGYGTVDAPLGLLNNEKACKDITDGGKINFK 480
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OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: April 26, 2005, 17:50:51 ; Search time 237.753 Seconds
                                              (without alignments)
                                              3624.358 Million cell updates/sec

Title: US-09-508-967-1
Perfect score: 12100
Sequence: 1 MATSGGSGGTQDEDAKHVLD..........VNNKKEIFEEEYPISDIWNI 2228

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_16Dec04:*
                 1: geneseqp1980s:*
                 2: geneseqp1990s:*
                 3: geneseqp2000s:*
                 4: geneseqp2001s:*
                 5: geneseqp2002s:*
                 6: geneseqp2003as:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	12100	100.0	2228	2	Aaw93944	Aaw93944 P. falcip
2	5074	41.9	2197	2	Aab18352	Aab18352 Plasmodiu
3	4817	39.8	2182	3	Aaw22476	Aaw22476 Plasmodiu
4	4817	39.8	2182	3	Aay77906	Aay77906 Plasmodiu
5	4802	39.7	3060	3	Aaw22475	Aaw22475 Plasmodiu
6	4802	39.7	3060	3	Aay77905	Aay77905 Plasmodiu
7	4084	33.8	2647	8	Adp25446	Adp25446 Plasmodiu
8	3928.5	32.5	2913	2	Aaw00384	Aaw00384 Plasmodiu
9	3197.5	26.4	2703	2	Aar70236	Aar70236 P. falcip
10	3197.5	26.4	2710	2	Aaw22482	Aaw22482 Plasmodiu
11	3197.5	26.4	2710	2	Aay77904	Aay77904 P. falcip
12	2929.5	24.2	1726	2	Aaw00385	Aaw00385 Truncated
13	2497	20.6	1700	3	Aab18144	Aab18144 Plasmodiu
14	1681.5	13.9	3542	4	Aab62142	Aab62142 P. falcip
15	1555	12.9	2459	8	Ado69969	Ado69969 Plasmodiu
16	1529.5	12.6	3056	8	Adr43499	Adr43499 CSA-bindi
17	1385	11.4	700	2	Aar70235	Aar70235 P. falcip
18	1385	11.4	700	2	Aaw22481	Aaw22481 Plasmodiu
19	1385	11.4	700	3	Aay77903	Aay77903 P. falcip
20	1319.5	10.9	431	3	Aab18350	Aab18350 Plasmodiu
21	782	6.5	440	3	Aab18146	Aab18146 Plasmodiu
22	702	5.8	921	2	Aaw22480	Aaw22480 Plasmodiu
23	702	5.8	921	2	Aay77902	Aay77902 P. falcip
24	697	5.8	793	2	Aar70234	Aar70234 P. falcip
25	624	5.2	302	8	Ado69970	Ado69970 Plasmodiu
26	591	4.9	445	4	Aab66344	Aab66344 Malarial
27	449	3.7	437	8	Ado69975	Ado69975 Plasmodiu
28	445	3.7	311	4	Aab62150	Aab62150 P. falcip
29	439.5	3.6	407	4	Aab62148	Aab62148 P. falcip
30	428.5	3.5	1604	2	Aar70105	Aar70105 P. falcip
31	425	3.5	1786	4	Aar41043	Aar41043 CD4-EBA17
32	422	3.5	294	4	Aab62147	Aab62147 P. falcip
33	421.5	3.5	1421	5	Aau76764	Aau76764 Plasmodiu
34	418	3.5	1435	2	Aar70232	Aar70232 P. falcip
35	418	3.5	1435	2	Aaw22477	Aaw22477 Sialic ac
36	418	3.5	1435	3	Aay77900	Aay77900 P. falcip
37	406	3.4	248	3	Aab18151	Aab18151 Plasmodiu
38	396	3.3	1086	5	Aau76760	Aau76760 Plasmodiu
39	386	3.2	308	4	Aab62151	Aab62151 P. falcip
40	382.5	3.2	301	8	Ado69973	Ado69973 Plasmodiu
41	379.5	3.1	362	4	Aay77912	Aay77912 Plasmodiu
42	377.5	3.1	245	8	Ado69972	Ado69972 Plasmodiu
43	376	3.1	1501	5	Aau76762	Aau76762 Plasmodiu
44	376	3.1	1501	5	Abp70152	Abp70152 Amino aci
45	375	3.1	351	4	Aab62149	Aab62149 P. falcip

ALIGNMENTS

RESULT 1
AAW93944
ID   AAW93944 standard; protein; 2228 AA.
XX
AC   AAW93944;
XX
DT   30-JUN-1999 (first entry)
XX
DE   P. falciparum PfEMP1 protein.
XX
KW   Erythrocyte, membrane protein; EMP.; PfEMP1; malaria; antiocclusional;
KW   glycosamino-glycan-like moiety; antiaggregational; antimalarial;
KW   antigen receptor; infected erythrocyte; rosette formation; blood cell;
KW   capillary occlusion; cerebral malaria; treatment; vaccine; detection;
KW   medicament; parasite; diagnosis; drug screening.
OS   Plasmodium falciparum.
XX
PN   WO9915557-A1.
XX
PD   01-APR-1999.
XX
PF   18-SEP-1998; 98WO-SE001675.
XX
PR   19-SEP-1997; 97SE-00003386.
XX
PA   (KARO-) KAROLINSKA INNOVATIONS AB.
XX
PI   Wahlgren M, Barragan A, Carlson J, Qijun C, Fernandez V;
XX
DR   WPI; 1999-254692/21.
XX
PT   New isolated malaria polypeptides.
XX
PS   Claim 4; Page 67-74; 80pp; English.
XX
CC   This invention describes a novel Plasmodium falciparum erythrocyte
CC   membrane protein (EMP), PfEMP1, which is capable of binding to a
CC   carbohydrate which exhibits at least one negatively charged glycosamino-
CC   glycan (GAG)-like moiety and has antiaggregational, antiocclusional and
CC   antimalarial activity. The carbohydrates of the invention are capable of
CC   acting as receptors for malaria antigens present on the surfaces of
CC   malaria infected erythrocytes, by binding to these antigens the
CC   carbohydrates prevent rosette formation by the blood cells, this prevents
CC   occlusion of capillaries as is seen in cerebral malaria caused by
CC   Plasmodium falciparum. The products of the invention can be used to treat
CC   malaria or to vaccinate against it, or used to design a model to identify
CC   compounds that bind to PfEMP1. The carbohydrates, polypeptides and